BIOINFORMATICS

How to cluster biological data?

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Outline

Gene expression and clustering;

Clustering as optimization problem;

In the second second

Hierarchical Clustering.

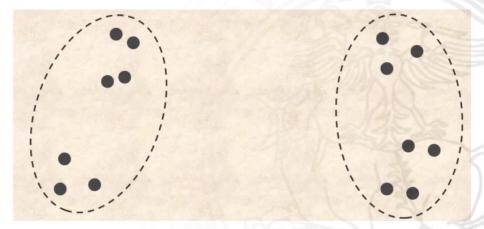
Chapter 8 in Bioinformatics Algorithms: An active Learning Approach (Vol.2).

Part 1 Hierarchical Clustering

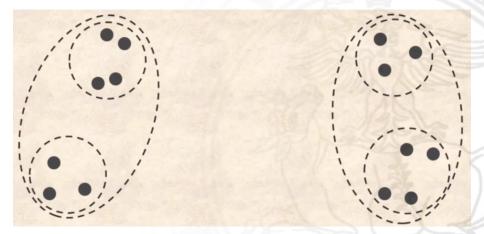
Stratification of Clusters



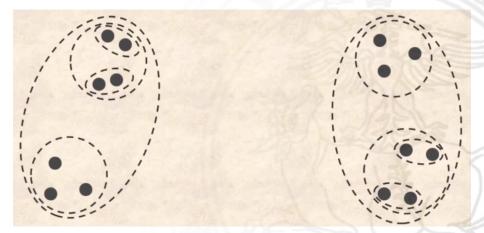
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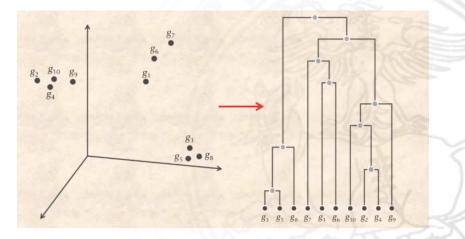


Stratification of Clusters



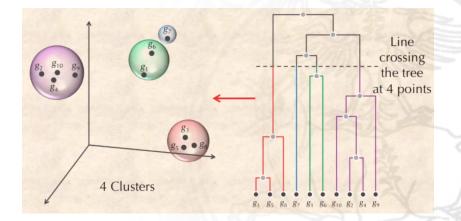
From Data to a Tree

• To capture stratification, the hierarchical clustering algorithm organizes *n* data points into a tree (namely Dendrogram).



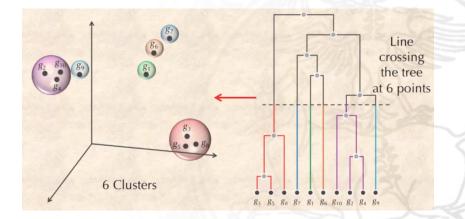
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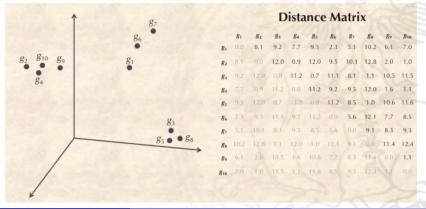
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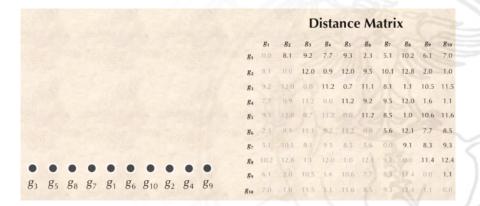
Constructing the Tree

- Hierarchical clustering starts from a trasformation of n × m expression matrix into n × n similarity matrix or Distance matrix;
- it can be obtained by simply computing Euclidean/Manhattan distance between genes.



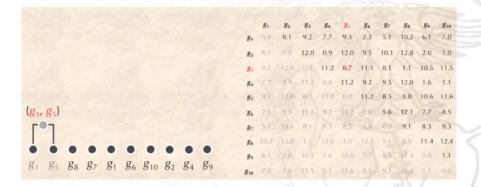
Constructing the Tree

• Create a node (i.e. a single element cluster) for every gene.



Constructing the Tree

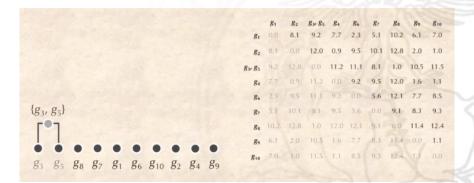
• Identify the two *closest* clusters and merge them.



Constructing the Tree

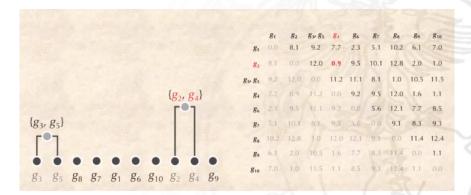
• Recompute the distance between two clusters as the minimal distance between the elements in the clusters:

$$D(C_1, C_2) = \min_{\forall i \in C_1, j \in C_2} D_{i,j}$$



Constructing the Tree

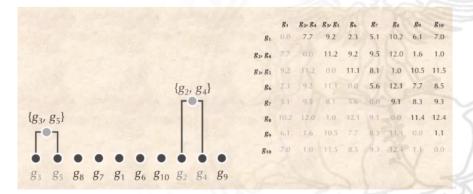
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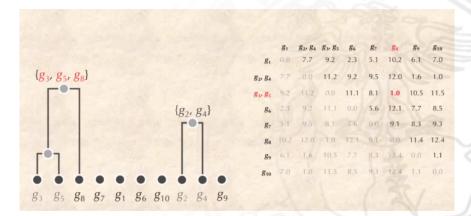
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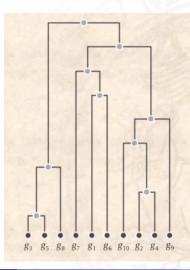
Constructing the Tree

• Identify the two *closest* clusters and merge them.



Constructing the Tree

• Iterate until all elements form a single cluster(i.e. root).



Constructing the Tree

HierarchicalClustering (D, n) Clusters $\leftarrow n$ single-element clusters labeled 1 to n $T \leftarrow$ a graph with the *n* isolated nodes labeled 1 to *n* while there is more than one cluster find the two closest clusters C_i and C_i merge C_i and C_i into a new cluster C_{new} with $|C_i| + |C_i|$ elements add a new node labeled by cluster Cnew to T connect node C_{new} to C_i and C_i by directed edges remove the rows and columns of D corresponding to C_i and C_i remove C_i and C_i from Clusters add a row and column to D for the cluster C_{new} by computing $D(C_{pew}, C)$ for each cluster C in Clusters add C_{new} to Clusters assign root in T as a node with no incoming edges return T

Different distance functions

Minimum distance between elements of two clusters: $D_{\min}(C_1, C_2) = \min_{\text{all points } i \text{ and } j \text{ in clusters } C1 \text{ and } C2, \text{ respectively } D_{i,j}$

Average distance between elements of two clusters:

 $D_{\text{avg}}(C_1, C_2) = (\sum_{\text{all points } i \text{ and } j \text{ in clusters } C_1 \text{ and } C_2, \text{ respectively } D_{i,j}) / (|C_1| * |C_2|)$

Difference between K-means and Hierarchical clustering

- Hierarchical clustering can not handle big data as well as K-means clustering.
- In K-means clustering, since we start with random choice of clusters, the results produced by running the algorithm multiple times might differ. While results are reproducible in Hierarchical clustering;
- K-means clustering requires prior knowledge of K.

Exercises

- Try to apply K-means algorithm on the following inputs:
 - ► *k* = 3;
 - ▶ $P_1(1,1)$, $P_2(2,1)$, $P_3(3,4)$, $P_4(1,6)$ $P_5(2,3)$, $P_6(3,3)$, $P_7(4,5)$, $P_8(2,5)$.
- Try to apply hierarchical clustering algorithm on the same input points.

		g_1	g ₂	g ₃	<i>g</i> 4	g 5	g 6	g7	g 8
$\mathcal{M}D =$	g_1	/0.000	1.000	3.605	5.000	2.236	2.828	5.000	4.123
	g_2	1.000	0.000	3.162	5.099	2.000	2.236	4.472	4.000
	g ₃	3.605	3.162	0.000	2.828	1.414	1.000	1.414	1.414
	g ₄	5.000	5.099	2.828	0.000	3.162	3.605	3.162	1.414
	g_5	2.236	2.000	1.414	3.162	0.000	1.000	2.828	2.000
	g_6	2.828	2.236	1.000	3.605	1.000	0.000	2.236	2.236
	g ₇	5.000	4.472	1.414	3.162	2.828	2.000	0.000	2.000
	g_8	4.123	4.000	1.414	1.414	2.000	2.236	2.000	0.000/